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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/776,696

DATE: 07/30/2001
TIME: 15:52:01

Input Set : N:\CrF3\RULE60\09776696.txt
Output Set: N:\CRF3\07302001\I776696.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Zhou, Shibin
 6 Zawel, Leigh
 7 Vogelstein, Bert
 8 Kinzler, Kenneth
 10 (ii) TITLE OF INVENTION: Human Fast-1 Gene
 13 (iii) NUMBER OF SEQUENCES: 18
 15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: Banner & Witcoff
 17 (B) STREET: 1001 G Street, NW
 18 (C) CITY: Washington
 19 (D) STATE: DC
 20 (E) COUNTRY: USA
 21 (F) ZIP: 20001
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Diskette
 25 (B) COMPUTER: IBM Compatible
 26 (C) OPERATING SYSTEM: DOS
 27 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/09/776,696
 C--> 31 (B) FILING DATE: 06-Feb-2001
 32 (C) CLASSIFICATION:
 34 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: 09/113,309
 36 (B) FILING DATE:
 40 (viii) ATTORNEY/AGENT INFORMATION:
 41 (A) NAME: Kagan, Sarah A
 42 (B) REGISTRATION NUMBER: 32141
 43 (C) REFERENCE/DOCKET NUMBER: 01107.10898
 45 (ix) TELECOMMUNICATION INFORMATION:
 46 (A) TELEPHONE: 202-508-9100
 47 (B) TELEFAX: 202-508-9299
 48 (C) TELEX:
 51 (2) INFORMATION FOR SEQ ID NO: 1:
 53 (i) SEQUENCE CHARACTERISTICS:
 54 (A) LENGTH: 1793 base pairs
 55 (B) TYPE: nucleic acid
 56 (C) STRANDEDNESS: single
 57 (D) TOPOLOGY: linear
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 62 GTTGAGTCAA TGTGTCCCCC TCTTGTTCCT AGGGTGCAGGG CTTCATGGCC TTCTCCTCCA 60
 63 GGAAGCTCCA CCTGATCATG TCCTGGGTGG ATATCCAGCC CCCATAGTTC AGGGCCTACT 120
 64 AGCAGCTGCT AGATCTTGAA CTCCAGGAGC GCCCCACGCC TTGGGAGCTT GGCATGGGCT 180
 65 AAATACTCCC CCATTGTGA AATGGGGTCC TGAACCTGA CCAGGGAAAGA CGGGATAAAG 240
 66 TAGCCATGGG TCATCGCAGC CCCTTGAAG CGGGCCTGG CCACCCAAAG GCAACTCAGG 300

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67	GGTGGAGACT	GAGGCCTCAG	GAGAAGCCCC	CACTAGAATG	CTCTCTGCC	CTCCCTTCCA	360
68	GATTAACCAA	AACCTGCTAA	TTGTGGAAGC	CCTCGGCATG	CTCCCCTCCC	CCACAGCCTC	420
69	TTCCTCCCTT	CCCTCCCCTC	CCCCTTCCAT	CCGAATGATA	AAGGCCAG	CCCGCCTGCC	480
70	CCAGCCCGGC	CTCAGGTCCC	GGCCCTGCCT	TCTACACTGC	CCCACCGCCC	TGCACCCCTCC	540
71	ACCCGGCCAG	GCCCCCTGCC	ACGCTGTCTA	CCGTCCCGCA	TGGGGCCCTG	CAGCGGCTCC	600
72	CGCCTGGGGC	CCCCAGAGGC	AGAGTCGCC	TCCCAGCCCC	CTAAGAGGAG	GAAGAAGAGG	660
73	TACCTGCGAC	ATGACAAGCC	CCCCTACACC	TACTTGGCCA	TGATGCCTT	GGTGATTCA	720
74	GCCGCTCCCT	CCCGCAGACT	GAAGCTGCC	CAGATCATCC	GTCAGGTCCA	GGCCGTGTT	780
75	CCCTTCTTCA	GGGAAGACTA	CGAGGGCTGG	AAAGACTCCA	TTCGCCACAA	CCTTCCTCC	840
76	AACCGATGCT	TCCGCAAGGT	GCCCAAGGAC	CCTGCAAAGC	CCCAGGCCAA	GGGCAACTTC	900
77	TGGGCGGTCTG	ACGTGAGCCT	GATCCCAGCT	GAGGCAGCTCC	GGCTGCAGAA	CACCGCCCTG	960
78	TGCCGGCGCT	GGCAGAACGG	AGGTGCGCGT	GGAGCCTCTG	CCAAGGACCT	GGGCCCCCTAC	1020
79	GTGCTGCACG	GCCGGCCATA	CCGGCCGCC	AGTCCCCCGC	CACCACCCAG	TGAGGGCTTC	1080
80	AGCATCAAGT	CCCTGCTAGG	AGGGTCCGGG	GAGGGGGCAC	CCTGGCCGGG	GCTAGCTCCA	1140
81	CAGAGCAGCC	CAGTTCTGC	AGGCACAGGG	AACAGTGGGG	AGGAGGGGT	GCCCCACCCCCA	1200
82	CCCCCTCCCT	CTTCTGAGAG	GCCTCTGTGG	CCCCCTCTGCC	CCCTTCCTGG	CCCCACGAGA	1260
83	GTGGAGGGGG	AGACTGTGCA	GGGGGGAGCC	ATCAGGGCCCT	CAACCCCTCTC	CCCAGAGCCT	1320
84	AGGGCCTGGC	CTCTCCACTT	ACTGCAGGGC	ACCGCAGTTC	CTGGGGGACG	GTCCAGCGGG	1380
85	GGACACAGGG	CCTCCCTCTG	GGGGCAGCTG	CCCACCTCCT	ACTTGCTAT	CTACACTCCC	1440
86	AATGTGGTAA	TGCCCTTGGC	ACCACCACCC	ACCTCTGTGTC	CCCAGTGTCC	GTCAACCCAGC	1500
87	CCTGCCTACT	GGGGGGTGGC	CCCTGAAACC	CGAGGGCCCC	CAGGGCTGCT	CTGCGATCTA	1560
88	GACGCCCTCT	TCCAAGGGGT	GCCACCCAAC	AAAAGCATCT	ACGACGTTG	GGTCAGGCCAC	1620
89	CCTCGGGACC	TGGCGGCC	TGGCCCAGGC	TGGCTGCTCT	CCTGGTGCA	CCTGTGAGGC	1680
90	TCTTAAGACA	GGGGCCGCTC	CTCCCCTCCCG	CTCCCACCCC	CACCTTGTG	ACAGGGAGCA	1740
91	AGGGAGGC	CTGTCTGCGA	CACAGCAGCT	CGAAAACCAG	GCAGAGCTTG	TTG	1793

93 (2) INFORMATION FOR SEQ ID NO: 2:

95 (i) SEQUENCE CHARACTERISTICS:

- 96 (A) LENGTH: 365 amino acids
- 97 (B) TYPE: amino acid
- 98 (C) STRANDEDNESS: single
- 99 (D) TOPOLOGY: linear

102 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

104	Met	Gly	Pro	Cys	Ser	Gly	Ser	Arg	Leu	Gly	Pro	Pro	Glu	Ala	Glu	Ser
105	1			5				10				15				
106	Pro	Ser	Gln	Pro	Pro	Lys	Arg	Arg	Lys	Lys	Arg	Tyr	Leu	Arg	His	Asp
107				20				25				30				
108	Lys	Pro	Pro	Tyr	Thr	Tyr	Leu	Ala	Met	Ile	Ala	Leu	Val	Ile	Gln	Ala
109				35				40				45				
110	Ala	Pro	Ser	Arg	Arg	Leu	Lys	Leu	Ala	Gln	Ile	Ile	Arg	Gln	Val	Gln
111				50				55				60				
112	Ala	Val	Phe	Pro	Phe	Arg	Glu	Asp	Tyr	Glu	Gly	Trp	Lys	Asp	Ser	
113				65				70			75			80		
114	Ile	Arg	His	Asn	Leu	Ser	Ser	Asn	Arg	Cys	Phe	Arg	Lys	Val	Pro	Lys
115					85				90				95			
116	Asp	Pro	Ala	Lys	Pro	Gln	Ala	Lys	Gly	Asn	Phe	Trp	Ala	Val	Asp	Val
117				100				105				110				
118	Ser	Leu	Ile	Pro	Ala	Glu	Ala	Leu	Arg	Leu	Gln	Asn	Thr	Ala	Leu	Cys
119				115				120				125				
120	Arg	Arg	Trp	Gln	Asn	Gly	Gly	Ala	Arg	Gly	Ala	Phe	Ala	Lys	Asp	Leu

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121 130 135 140
122 Gly Pro Tyr Val Leu His Gly Arg Pro Tyr Arg Pro Pro Ser Pro Pro
123 145 150 155 160
124 Pro Pro Pro Ser Glu Gly Phe Ser Ile Lys Ser Leu Leu Gly Gly Ser
125 165 170 175
126 Gly Glu Gly Ala Pro Trp Pro Gly Leu Ala Pro Gln Ser Ser Pro Val
127 180 185 190
128 Pro Ala Gly Thr Gly Asn Ser Gly Glu Ala Val Pro Thr Pro Pro
129 195 200 205
130 Leu Pro Ser Ser Glu Arg Pro Leu Trp Pro Leu Cys Pro Leu Pro Gly
131 210 215 220
132 Pro Thr Arg Val Glu Gly Glu Thr Val Gln Gly Gly Ala Ile Gly Pro
133 225 230 235 240
134 Ser Thr Leu Ser Pro Glu Pro Arg Ala Trp Pro Leu His Leu Leu Gln
135 245 250 255
136 Gly Thr Ala Val Pro Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser
137 260 265 270
138 Leu Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn
139 275 280 285
140 Val Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro
141 290 295 300
142 Ser Thr Ser Pro Ala Tyr Trp Gly Val Ala Pro Glu Thr Arg Gly Pro
143 305 310 315 320
144 Pro Gly Leu Leu Cys Asp Leu Asp Ala Leu Phe Gln Gly Val Pro Pro
145 325 330 335
146 Asn Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala
147 340 345 350
148 Ala Pro Gly Pro Gly Trp Leu Leu Ser Trp Cys Ser Leu
149 355 360 365

151 (2) INFORMATION FOR SEQ ID NO: 3:

153 (i) SEQUENCE CHARACTERISTICS:
154 (A) LENGTH: 477 amino acids
155 (B) TYPE: amino acid
156 (C) STRANDEDNESS: single
157 (D) TOPOLOGY: linear

160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

162 Val Ala Met Ile Asn Ala Cys Ile Asp Ser Met Ser Ser Ile Leu Pro
163 1 5 10 15
164 Phe Thr Pro Pro Val Val Lys Arg Leu Leu Gly Trp Lys Lys Ser Ala
165 20 25 30
166 Gly Gly Ser Gly Gly Ala Gly Gly Glu Gln Asn Gly Gln Glu Glu
167 35 40 45
168 Lys Trp Cys Glu Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys
169 50 55 60
170 Thr Gly Arg Leu Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Cys
171 65 70 75 80
172 Asn Thr Lys Cys Val Thr Ile Pro Ser Thr Cys Ser Glu Ile Trp Gly
173 85 90 95
174 Leu Ser Thr Pro Asn Thr Ile Asp Gln Trp Asp Thr Thr Gly Leu Tyr

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175	100	105	110
176	Ser Phe Ser Glu Gln Thr Arg Ser	Leu Asp Gly Arg	Leu Gln Val Ser
177	115	120	125
178	His Arg Lys Gly Leu Pro His	Val Ile Tyr Cys Arg	Leu Trp Arg Trp
179	130	135	140
180	Pro Asp Leu His Ser His	Glu Leu Lys Ala Ile	Glu Asn Cys Glu
181	145	150	155
182	Tyr Ala Phe Asn Leu Lys	Asp Glu Val Cys Val Asn	Pro Tyr His
183	165	170	175
184	Tyr Gln Arg Val Glu Thr Pro	Val Leu Pro Pro Val	Leu Val Pro Arg
185	180	185	190
186	His Thr Glu Ile Leu Thr	Glu Leu Pro Pro Leu Asp	Asp Tyr Thr His
187	195	200	205
188	Ser Ile Pro Glu Asn Thr	Asn Phe Pro Ala Gly	Ile Glu Pro Gln Ser
189	210	215	220
190	Asn Tyr Ile Pro Glu Thr	Pro Pro Pro Gly Tyr	Ile Ser Glu Asp Gly
191	225	230	235
192	Glu Thr Ser Asp Gln Gln	Leu Asn Gln Ser	Met Asp Thr Gly Ser Pro
193	245	250	255
194	Ala Glu Leu Ser Pro Thr	Thr Leu Ser Pro Val	Asn His Ser Leu Asp
195	260	265	270
196	Leu Gln Pro Val Thr Tyr	Ser Glu Pro Ala Phe	Trp Cys Ser Ile Ala
197	275	280	285
198	Tyr Tyr Glu Leu Asn Gln	Arg Val Gly Glu Thr	Phe His Ala Ser Gln
199	290	295	300
200	Pro Ser Leu Thr Val Asp	Gly Phe Thr Asp Pro	Ser Asn Ser Glu Arg
201	305	310	315
202	Phe Cys Leu Gly	Leu Leu Ser Asn Val	Asn Arg Asn Ala Thr Val Glu
203	325	330	335
204	Met Thr Arg Arg His	Ile Gly Arg Gly Val	Arg Leu Tyr Tyr Ile Gly
205	340	345	350
206	Gly Glu Val Phe Ala Glu	Cys Leu Ser Asp Ser	Ala Ile Phe Val Gln
207	355	360	365
208	Ser Pro Asn Cys Asn Gln	Arg Tyr Gly Trp His	Pro Ala Thr Val Cys
209	370	375	380
210	Lys Ile Pro Pro Gly	Cys Asn Leu Lys Ile	Phe Asn Asn Gln Glu Phe
211	385	390	395
212	405	410	415
213	Gln Leu Thr Arg Met Cys	Thr Ile Arg Met Ser	Phe Val Lys Gly Trp
214	420	425	430
215	Gly Ala Glu Tyr Arg Arg	Gln Thr Val Thr Ser	Thr Pro Cys Trp Ile
216	435	440	445
217	Glu Leu His Leu Asn Gln	Pro Leu Gln Trp Leu Asp	Lys Val Leu Thr
218	450	455	460
219	Gln Met Gly Ser Pro Ser	Val Arg Cys Ser	Ser Met Ser
220	465	470	475
221	(2) INFORMATION FOR SEQ ID NO: 4:		
222	(i) SEQUENCE CHARACTERISTICS:		

RAW SEQUENCE LISTING
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Input Set : N:\Crf3\RULE60\09776696.txt
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226	(A) LENGTH: 8 base pairs	
227	(B) TYPE: nucleic acid	
228	(C) STRANDEDNESS: single	
229	(D) TOPOLOGY: linear	
232	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:	
234	TGKKATT	8
236	(2) INFORMATION FOR SEQ ID NO: 5:	
238	(i) SEQUENCE CHARACTERISTICS:	
239	(A) LENGTH: 18 base pairs	
240	(B) TYPE: nucleic acid	
241	(C) STRANDEDNESS: single	
242	(D) TOPOLOGY: linear	
245	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:	
247	CTGGAAAGAC TCCATTG	18
249	(2) INFORMATION FOR SEQ ID NO: 6:	
251	(i) SEQUENCE CHARACTERISTICS:	
252	(A) LENGTH: 19 base pairs	
253	(B) TYPE: nucleic acid	
254	(C) STRANDEDNESS: single	
255	(D) TOPOLOGY: linear	
258	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:	
260	CACAGAGGCC TCTCAGAAG	19
262	(2) INFORMATION FOR SEQ ID NO: 7:	
264	(i) SEQUENCE CHARACTERISTICS:	
265	(A) LENGTH: 18 base pairs	
266	(B) TYPE: nucleic acid	
267	(C) STRANDEDNESS: single	
268	(D) TOPOLOGY: linear	
271	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
273	CCCCCTTCCA TCCGAATG	18
275	(2) INFORMATION FOR SEQ ID NO: 8:	
277	(i) SEQUENCE CHARACTERISTICS:	
278	(A) LENGTH: 19 base pairs	
279	(B) TYPE: nucleic acid	
280	(C) STRANDEDNESS: single	
281	(D) TOPOLOGY: linear	
284	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
286	GAGCTGCTGT GTCGAGAC	19
288	(2) INFORMATION FOR SEQ ID NO: 9:	
290	(i) SEQUENCE CHARACTERISTICS:	
291	(A) LENGTH: 79 base pairs	
292	(B) TYPE: nucleic acid	
293	(C) STRANDEDNESS: single	
294	(D) TOPOLOGY: linear	
297	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
299	GGATCTTAAT ACGACTCACT ATAGGGAGAC CACCATGGAC TACAAGGACG ACGATGACAA	60
300	GGGGCCCTGC AGCGGCTCC	79
302	(2) INFORMATION FOR SEQ ID NO: 10:	
304	(i) SEQUENCE CHARACTERISTICS:	

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/776,696

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Input Set : N:\Crf3\RULE60\09776696.txt
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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]